SEQUENCE LISTING

<110> Matuschek, Markus
Heinekamp, Thorsten
Schmidt, Andre
Brakhage, Axel

<120> Method for the genetic modification of organisms of the genus Blakeslea, corresponding organisms, and the use of the same

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<140> US 10/541,993
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<150> PCT/EP2004/000100
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<220>
<223> Primer

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<210> 6
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<220>
<223> Primer

<400> 6
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<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
tgagaatatc accggaattg 20

<210> 8
<211> 21
<212> DNA
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<220>
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<400> 8
agctcgacat actgttcttc c 21

<210> 9
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<220>
<223> Primer

<400> 9
gtgaatggaa atcccatcgc tgtc 24

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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
agtgggtact ctaaaggcca tacc 24

<210> 11
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<212> DNA
<213> Haematococcus pluvialis

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<222> (166)..(1155)

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ccgcgagtct cccgccgcac tgactgccat agcacagcta gacga atg cag cta gca    177
                                                  Met Gln Leu Ala
                                                  1

gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag      225
Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys
5                   10                  15                  20

gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg      273
Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp
                25                  30                  35

gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg      321
Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro
            40                  45                  50

gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc      369
Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile
        55                  60                  65

aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac      417
Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His
    70                  75                  80

gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg      465
Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp
85                  90                  95                  100

ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc      513
Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser
                105                 110                 115

ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca      561
Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr
            120                 125                 130

ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg      609
Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met
        135                 140                 145

aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg      657
Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu
    150                 155                 160

tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac      705
Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His
165                 170                 175                 180

cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga      753
His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly
                185                 190                 195

aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg      801
Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met
            200                 205                 210

tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag      849
Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln
```

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        215                 220                 225

ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg      897
Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala
    230                 235                 240

ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc      945
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro
245                 250                 255                 260

cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg      993
His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met
                265                 270                 275

aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt     1041
Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe
            280                 285                 290

ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc     1089
Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro
        295                 300                 305

ttc gcc ccc tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga     1137
Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg
    310                 315                 320

ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc cctgctgcca            1185
Gly Leu Val Pro Ala
325

gctgggcatg caggttgtgg caggactggg tgaggtgaaa agctgcaggc gctgctgccg   1245

gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg tttgtagctg   1305

tcgagcttgc cccatggatg aagctgtgta gtggtgcagg gagtacaccc acaggccaac   1365

acccttgcag gagatgtctt gcgtcgggag gagtgttggg cagtgtagat gctatgattg   1425

tatcttaatg ctgaagcctt taggggagcg acacttagtg ctgggcaggc aacgccctgc   1485

aaggtgcagg cacaagctag gctggacgag gactcggtgg caggcaggtg aagaggtgcg   1545

ggagggtggt gccacaccca ctgggcaaga ccatgctgca atgctggcgg tgtggcagtg   1605

agagctgcgt gattaactgg gctatggatt gtttgagcag tctcacttat tctttgatat   1665

agatactggt caggcaggtc aggagagtga gtatgaacaa gttgagaggt ggtgcgctgc   1725

ccctgcgctt atgaagctgt aacaataaag tggttcaaaa aaaaaa                  1771
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<210> 12
<211> 329
<212> PRT
<213> Haematococcus pluvialis

<400> 12

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Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
1               5                   10                  15
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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
            20                  25                  30

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
        35                  40                  45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
    50                  55                  60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
65                  70                  75                  80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
                85                  90                  95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
            100                 105                 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
        115                 120                 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
    130                 135                 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
145                 150                 155                 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
                165                 170                 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
            180                 185                 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
        195                 200                 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
    210                 215                 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
225                 230                 235                 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
                245                 250                 255
```

```
Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
            260                 265                 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
        275                 280                 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
    290                 295                 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
305                 310                 315                 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
                325
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<210> 13
<211> 1662
<212> DNA
<213> Haematococcus pluvialis

<220>
<221> CDS
<222> (168)..(1130)

<400> 13

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gctatcgacg tggttgtgag cgctcgacgt ggtccactga cgggcctgtg agcctctgcg     120

ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc       176
                                                    Met His Val
                                                    1

gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc       224
Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
    5                   10                  15

agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc       272
Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
20                  25                  30                  35

gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct       320
Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
                40                  45                  50

cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc       368
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
            55                  60                  65

acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg       416
Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
        70                  75                  80

aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc       464
Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
```

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    85                  90                  95

cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc      512
Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe
100                 105                 110                 115

att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac      560
Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp
                120                 125                 130

gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc      608
Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu
            135                 140                 145

ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg      656
Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met
        150                 155                 160

ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg      704
Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly
    165                 170                 175

aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc      752
Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe
180                 185                 190                 195

gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg      800
Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu
                200                 205                 210

gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat      848
Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn
            215                 220                 225

ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc      896
Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu
        230                 235                 240

ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca      944
Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala
    245                 250                 255

gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca      992
Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala
260                 265                 270                 275

tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg     1040
Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp
                280                 285                 290

gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc     1088
Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys
            295                 300                 305

cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga             1130
Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
        310                 315                 320

cctggtccct ccgctggtga cccagcgtct gcacaagagt gtcatgctac agggtgctgc   1190

ggccagtggc agcgcagtgc actctcagcc tgtatggggc taccgctgtg ccactgagca   1250
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ctgggcatgc cactgagcac tgggcgtgct actgagcaat gggcgtgcta ctgagcaatg 1310

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tgcattcagt agcggtggcc aacgtcatgt ggatggtgga agtgctgagg ggtttaggca 1430

gccggcattt gagagggcta agttataaat cgcatgctgc tcatgcgcac atatctgcac 1490

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gttttattca gcagcagtac ttagtgaggg tgagagcagg gtggtgagag tggagtgagt 1610

gagtatgaac ctggtcagcg aggtgaacag cctgtaatga atgactctgt ct 1662

<210> 14
<211> 320
<212> PRT
<213> Haematococcus pluvialis

<400> 14

Met His Val Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala
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Ala Ala Ser Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His
20 25 30

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
35 40 45

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
50 55 60

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
65 70 75 80

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
85 90 95

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
100 105 110

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
115 120 125

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
130 135 140

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
145 150 155 160

```
Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
                165                 170                 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
            180                 185                 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
        195                 200                 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
    210                 215                 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
225                 230                 235                 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
                245                 250                 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
            260                 265                 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
        275                 280                 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
    290                 295                 300

Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
305                 310                 315                 320
```

<210> 15
<211> 729
<212> DNA
<213> Agrobacterium aurantiacum

<220>
<221> CDS
<222> (1)..(729)

<400> 15

```
atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg       48
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1               5                   10                  15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat       96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
            20                  25                  30
```

```
gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca      144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
        35                  40                  45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg      192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
    50                  55                  60

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat      240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65                  70                  75                  80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg      288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
                85                  90                  95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc      336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
            100                 105                 110

gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc      384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
        115                 120                 125

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc      432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
    130                 135                 140

gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac      480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145                 150                 155                 160

gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc      528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
                165                 170                 175

gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg      576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
            180                 185                 190

gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg      624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
        195                 200                 205

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac      672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
    210                 215                 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac      720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225                 230                 235                 240

acc gca tga                                                          729
Thr Ala
```

<210> 16
<211> 242
<212> PRT
<213> Agrobacterium aurantiacum

<400> 16

```
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1               5                  10                  15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
            20                  25                  30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
        35                  40                  45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
    50                  55                  60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65                  70                  75                  80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
                85                  90                  95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
            100                 105                 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
        115                 120                 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
    130                 135                 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145                 150                 155                 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
                165                 170                 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
            180                 185                 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
        195                 200                 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
    210                 215                 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225                 230                 235                 240
```

Thr Ala

<210> 17
<211> 1631
<212> DNA
<213> Alcaligenes sp.

<220>
<221> CDS
<222> (99)..(827)

<400> 17
ctgcaggccg ggcccggtgg ccaatggtcg caaccggcag gactggaaca ggacggcggg 60

ccggtctagg ctgtcgccct acgcagcagg agtttcgg atg tcc gga cgg aag cct 116
Met Ser Gly Arg Lys Pro
1 5

ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164
Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile
10 15 20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212
Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp
25 30 35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260
Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr
40 45 50

tgg ctg tcg gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308
Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly
55 60 65 70

tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg 356
Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu
75 80 85

gcg ctg tgg ctc tat gcg ggg ttc tcg tgg ccc aag ctg atc gcc aag 404
Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys
90 95 100

cac atg acg cat cac cgg cac gcc ggc acc gac aac gat ccc gat ttc 452
His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe
105 110 115

ggt cac gga ggg ccc gtg cgc tgg tac ggc agc ttc gtc tcc acc tat 500
Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr
120 125 130

ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat 548
Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr
135 140 145 150

gcg ctg atc ctg ggc gat cgc tgg atg tat gtc atc ttc tgg ccg gtc 596
Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val

```
                155                 160                 165

ccg gcc gtt ctg gcg tcg atc cag att ttc gtc ttc gga act tgg ctg      644
Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu
            170                 175                 180

ccc cac cgc ccg gga cat gac gat ttt ccc gac cgg cac aac gcg agg      692
Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg
        185                 190                 195

tcg acc ggc atc ggc gac ccg ttg tca cta ctg acc tgc ttc cat ttc      740
Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Thr Cys Phe His Phe
    200                 205                 210

ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg      788
Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp
215                 220                 225                 230

cgc ctg cct cgt aca cgc aag acc gga ggc cgc gca tga cgcaattcct       837
Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly Arg Ala
                235                 240

cattgtcgtg gcgacagtcc tcgtgatgga gctgaccgcc tattccgtcc accgctggat    897

tatgcacggc cccctaggct ggggctggca caagtcccat cacgaagagc acgaccacgc    957

gttggagaag aacgacctct acggcgtcgt cttcgcggtg ctggcgacga tcctcttcac   1017

cgtgggcgcc tattggtggc cggtgctgtg gtggatcgcc ctgggcatga cggtctatgg   1077

gttgatctat ttcatcctgc acgacgggct tgtgcatcaa cgctggccgt ttcggtatat   1137

tccgcggcgg ggctatttcc gcaggctcta ccaagctcat cgcctgcacc acgcggtcga   1197

ggggcgggac cactgcgtca gcttcggctt catctatgcc ccacccgtgg acaagctgaa   1257

gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgtccgt cgtgatctct   1317

gatcccggcg tggccgcatg aaatccgacg tgctgctggc aggggccggc cttgccaacg   1377

gactgatcgc gctggcgatc cgcaaggcgc ggcccgacct tcgcgtgctg ctgctggacc   1437

gtgcggcggg cgcctcggac gggcatactt ggtcctgcca cgacaccgat ttggcgccgc   1497

actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt   1557

tcccagacca ttcgcgaagg ctccgggccg gatatggctc gatcgacggg cgggggctga   1617

tgcgtgcggt gacc                                                     1631
```

<210> 18
<211> 242
<212> PRT
<213> Alcaligenes sp.

<400> 18

```
Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
1               5                   10                  15
```

```
Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
            20                  25                  30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
        35                  40                  45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
    50                  55                  60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65                  70                  75                  80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
                85                  90                  95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
            100                 105                 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
        115                 120                 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
    130                 135                 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145                 150                 155                 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
                165                 170                 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
            180                 185                 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
        195                 200                 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
    210                 215                 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
225                 230                 235                 240

Arg Ala
```

<210> 19
<211> 729
<212> DNA
<213> Paracoccus marcusii

<220>
<221> CDS
<222> (1)..(729)

<400> 19

```
atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc aca agc ctg       48
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1               5                  10                  15

atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat       96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
            20                  25                  30

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg      144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
        35                  40                  45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg      192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
    50                  55                  60

cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat      240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65                  70                  75                  80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg      288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
                85                  90                  95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc      336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
            100                 105                 110

gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc      384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
        115                 120                 125

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc      432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
    130                 135                 140

gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac      480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145                 150                 155                 160

gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc      528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
                165                 170                 175

gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg      576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
            180                 185                 190

gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg      624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
```

```
        195                 200                 205

ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac      672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
    210                 215                 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac      720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225                 230                 235                 240

acc gca tga                                                          729
Thr Ala
```

<210> 20
<211> 242
<212> PRT
<213> Paracoccus marcusii

<400> 20

```
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1               5                   10                  15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
            20                  25                  30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
        35                  40                  45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
    50                  55                  60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65                  70                  75                  80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
                85                  90                  95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
            100                 105                 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
        115                 120                 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
    130                 135                 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145                 150                 155                 160
```

```
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
                165                 170                 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
            180                 185                 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
        195                 200                 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
    210                 215                 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225                 230                 235                 240

Thr Ala
```

<210> 21
<211> 1629
<212> DNA
<213> Synechocystis sp.

<220>
<221> CDS
<222> (1)..(1629)

<400> 21

```
atg atc acc acc gat gtt gtc att att ggg gcg ggg cac aat ggc tta       48
Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1               5                   10                  15

gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta       96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
            20                  25                  30

gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg      144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
        35                  40                  45

ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac      192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
    50                  55                  60

gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag      240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65                  70                  75                  80

tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg      288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
                85                  90                  95

ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt      336
```

```
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
            100                 105                 110

gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa      384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
        115                 120                 125

ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt      432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
    130                 135                 140

aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg      480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145                 150                 155                 160

gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg      528
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
                165                 170                 175

ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat      576
Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
            180                 185                 190

gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt      624
Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
        195                 200                 205

tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg      672
Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
    210                 215                 220

atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga      720
Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
225                 230                 235                 240

ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa      768
Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
                245                 250                 255

ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa      816
Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
            260                 265                 270

aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg      864
Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
        275                 280                 285

gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg      912
Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
    290                 295                 300

caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg      960
Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
305                 310                 315                 320

gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa     1008
Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
                325                 330                 335

atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg     1056
Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
```

```
                340                 345                 350

ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat     1104
Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
        355                 360                 365

gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct     1152
Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
    370                 375                 380

aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg     1200
Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
385                 390                 395                 400

gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac     1248
Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
                405                 410                 415

cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc     1296
Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
            420                 425                 430

gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg     1344
Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
        435                 440                 445

gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa     1392
Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
    450                 455                 460

agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc     1440
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
465                 470                 475                 480

tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta     1488
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
                485                 490                 495

ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca     1536
Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
            500                 505                 510

ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga     1584
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
        515                 520                 525

aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa         1629
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
    530                 535                 540
```

<210> 22
<211> 542
<212> PRT
<213> Synechocystis sp.

<400> 22

```
Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1               5                   10                  15
```

```
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
            20                  25                  30

Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
        35                  40                  45

Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
    50                  55                  60

Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65                  70                  75                  80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
                85                  90                  95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
            100                 105                 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
        115                 120                 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
    130                 135                 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145                 150                 155                 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
                165                 170                 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
            180                 185                 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
        195                 200                 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
    210                 215                 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
225                 230                 235                 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
                245                 250                 255
```

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr

```
            500                 505                 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
        515                 520                 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
    530                 535                 540
```

<210> 23
<211> 776
<212> DNA
<213> Bradyrhizobium sp.

<220>
<221> CDS
<222> (1)..(774)

<400> 23

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atg cat gca gca acc gcc aag gct act gag ttc ggg gcc tct cgg cgc       48
Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
1               5                   10                  15

gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc       96
Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
            20                  25                  30

atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg      144
Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
        35                  40                  45

ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag      192
Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
    50                  55                  60

acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac      240
Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65                  70                  75                  80

ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag      288
Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
                85                  90                  95

ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc      336
Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
            100                 105                 110

gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat      384
Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
        115                 120                 125

ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt      432
Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
    130                 135                 140

ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc      480
Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
145                 150                 155                 160
```

```
tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg      528
Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
                165                 170                 175

ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc      576
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
            180                 185                 190

ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat      624
Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
        195                 200                 205

cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg      672
Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
    210                 215                 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat      720
Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225                 230                 235                 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg      768
Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
                245                 250                 255

cgt gac ta                                                          776
Arg Asp
```

<210> 24
<211> 258
<212> PRT
<213> Bradyrhizobium sp.

<400> 24

```
Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
1               5                   10                  15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
            20                  25                  30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
        35                  40                  45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
    50                  55                  60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65                  70                  75                  80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
                85                  90                  95
```

```
Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
            100                 105                 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
        115                 120                 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
    130                 135                 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
145                 150                 155                 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
                165                 170                 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
            180                 185                 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
        195                 200                 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
    210                 215                 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225                 230                 235                 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
                245                 250                 255

Arg Asp
```

<210> 25
<211> 777
<212> DNA
<213> Nostoc sp.

<220>
<221> CDS
<222> (1)..(777)

<400> 25

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atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta      48
Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
1               5                   10                  15

ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt      96
Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
```

```
                20                  25                  30

att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta      144
Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
        35                  40                  45

ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc      192
Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
    50                  55                  60

atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat      240
Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
65                  70                  75                  80

gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat      288
Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
                85                  90                  95

ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa      336
Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
            100                 105                 110

gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat      384
Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
        115                 120                 125

tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg      432
Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
    130                 135                 140

tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga      480
Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
145                 150                 155                 160

tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa      528
Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
                165                 170                 175

aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta      576
Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
            180                 185                 190

caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt      624
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
        195                 200                 205

ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt      672
Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
    210                 215                 220

tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac      720
Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
225                 230                 235                 240

gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata      768
Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
                245                 250                 255

tct tta taa                                                         777
Ser Leu
```

<210> 26
<211> 258
<212> PRT
<213> Nostoc sp.

<400> 26

```
Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
1               5                  10                  15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
            20                  25                  30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
        35                  40                  45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
    50                  55                  60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
65                  70                  75                  80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
                85                  90                  95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
            100                 105                 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
        115                 120                 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
    130                 135                 140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
145                 150                 155                 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
                165                 170                 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
            180                 185                 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
        195                 200                 205
```

```
Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
    210                 215                 220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
225                 230                 235                 240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
                245                 250                 255

Ser Leu
```

<210> 27
<211> 789
<212> DNA
<213> Nostoc punctiforme

<220>
<221> CDS
<222> (1)..(789)

<400> 27

```
ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa       48
Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1               5                   10                  15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta       96
Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
            20                  25                  30

att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat      144
Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
        35                  40                  45

tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa      192
Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
    50                  55                  60

atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat      240
Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
65                  70                  75                  80

ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca      288
Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
                85                  90                  95

cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag      336
Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
            100                 105                 110

aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat      384
Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
        115                 120                 125

ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc      432
Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
```

```
    130                 135                 140

atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta      480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145                 150                 155                 160

ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc      528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
                165                 170                 175

tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat      576
Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
            180                 185                 190

ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat      624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
        195                 200                 205

ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc      672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
    210                 215                 220

gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat      720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225                 230                 235                 240

gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac      768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
                245                 250                 255

aat tca gta acc aat tcg taa                                          789
Asn Ser Val Thr Asn Ser
            260
```

<210> 28
<211> 262
<212> PRT
<213> Nostoc punctiforme

<400> 28

```
Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1               5                   10                  15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
            20                  25                  30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
        35                  40                  45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
    50                  55                  60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
65                  70                  75                  80
```

```
Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
                85                  90                  95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
            100                 105                 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
        115                 120                 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
    130                 135                 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145                 150                 155                 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
                165                 170                 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
            180                 185                 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
        195                 200                 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
    210                 215                 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225                 230                 235                 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
                245                 250                 255

Asn Ser Val Thr Asn Ser
            260
```

<210> 29
<211> 762
<212> DNA
<213> Nostoc punctiforme

<220>
<221> CDS
<222> (1)..(762)

<400> 29
gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca 48

```
Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
1               5                  10                  15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc      96
Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
            20                  25                  30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac     144
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
        35                  40                  45

atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa     192
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
    50                  55                  60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat     240
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65                  70                  75                  80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca     288
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
                85                  90                  95

ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa     336
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
            100                 105                 110

aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat     384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
        115                 120                 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt     432
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
    130                 135                 140

atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att     480
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145                 150                 155                 160

tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act     528
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
                165                 170                 175

tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat     576
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
            180                 185                 190

ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag     624
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
        195                 200                 205

cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc     672
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
    210                 215                 220

acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat     720
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225                 230                 235                 240

att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag              762
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
```

245 250

<210> 30
<211> 253
<212> PRT
<213> Nostoc punctiforme

<400> 30

Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
195 200 205

```
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
    210                 215                 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225                 230                 235                 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
                245                 250
```

<210> 31
<211> 1608
<212> DNA
<213> Haematococcus pluvialis

<220>
<221> CDS
<222> (3)..(971)

<400> 31

```
ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc        47
   Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
   1               5                   10                  15

ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg        95
Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
                20                  25                  30

tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc       143
Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
            35                  40                  45

cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg       191
Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
        50                  55                  60

tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga       239
Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly
    65                  70                  75

acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca       287
Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala
80                  85                  90                  95

ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa       335
Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys
                100                 105                 110

cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc       383
Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly
            115                 120                 125

gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac       431
Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His
        130                 135                 140

atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc       479
```

```
Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu
    145                 150                 155

ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat      527
Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr
160                 165                 170                 175

gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac      575
Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His
                180                 185                 190

aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg      623
Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu
            195                 200                 205

ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc      671
Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly
        210                 215                 220

ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg      719
Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu
    225                 230                 235

ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg      767
Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu
240                 245                 250                 255

gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg      815
Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met
                260                 265                 270

aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt      863
Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly
            275                 280                 285

ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att      911
Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile
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cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg      959
Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp
    305                 310                 315

tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg         1011
Ser Lys Arg
320

tgataaggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggtctga   1071

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Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
20 25 30

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35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
180 185 190

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Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
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Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
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Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
225                 230                 235                 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
                245                 250                 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
            260                 265                 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
        275                 280                 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
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Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
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Lys Arg
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atg gaa gtg att gct gca ctg gca cac aaa tac atc atg cac ggc tgg       96
Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
            20                  25                  30

ggt tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggt gcg ttt      144
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
        35                  40                  45

gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg      192
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Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
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ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc      240
Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
65                  70                  75                  80

gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggg      288
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
                85                  90                  95

ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac      336
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
            100                 105                 110

ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc      384
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
        115                 120                 125

aaa gaa ggt tgt gtt tct ttt ggc ttc ctc tat gcg ccg ccc ctg tca      432
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
    130                 135                 140

aaa ctt cag gcg acg ctc cgg gaa aga cat ggc gct aga gcg ggc gct      480
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
145                 150                 155                 160

gcc aga gat gcg cag ggc ggg gag gat gag ccc gca tcc ggg aag taa      528
Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys
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<212> PRT
<213> Erwinia uredovora

<400> 34

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1               5                   10                  15

Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
            20                  25                  30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
        35                  40                  45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
    50                  55                  60

Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
65                  70                  75                  80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
                85                  90                  95
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Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
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Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
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Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys
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